

IN THE CLAIMS

Please amend the claims as follows:

Claims 1-22 (Cancelled)

Claim 23 (Currently Amended): A method for assessing the risk of vesnarinone-  
induced drug-induced granulocytopenia comprising:

detecting in a subject in need thereof at least one polynucleotide polymorphism of the  
human insulin receptor substrate 2 gene in the polynucleotide sequence described by  
GenBank Accession No. AL162497 (version 20)(SEQ ID NO: 18) the human insulin receptor  
substrate-2 gene,

wherein the presence of a polymorphism correlates with the risk of vesnarinone-  
induced drug-induced granulocytopenia[[:]] and

wherein SEQ ID NO: 19 shows the polynucleotides of a human insulin receptor  
substrate-2 gene;

wherein said at least one polymorphism is a polymorphism A29793G that is a T to C  
conversion at position 96,095 of SEQ ID NO: 18.

Claim 24 (Cancelled)

Claim 25 (Previously Presented): The method of claim 23, wherein the genetic  
polymorphism is detected through at least one technique selected from the group consisting  
of allele-specific oligonucleotide (ASO)-dot blot analysis, single nucleotide primer extension  
assay, PCR-single strand conformation polymorphism (SSCP) analysis, Invader assay,

quantitative real-time PCR assay, and genetic polymorphism assay employing a mass spectrometer (mass array).

Claim 26 (Previously Presented): The method of claim 23, wherein the genetic polymorphism is detected through direct nucleotide sequencing.

Claim 27 (Previously Presented): The method of claim 23, wherein the genetic polymorphism is detected through PCR-restriction enzyme fragment length polymorphism (RFLP) analysis.

Claim 28 (Currently Amended): The method of claim 27, wherein the PCR-restriction enzyme fragment length polymorphism (RFLP) analysis is performed by use of the restriction enzyme *Afa* I for detecting [[A]] T to [[G]] C conversion at position [[47,315]] 96,095 of SEQ ID NO: 18 ~~SEQ ID NO: 19~~.

Claim 29 (Cancelled)

Claim 30 (Currently Amended): The method of claim 23, wherein said polymorphism is identified by a method employing a probe or primer selected from the group consisting of:

(a) an oligonucleotide having a sequence including a genetic polymorphism that is [[C]] G to [[A]] T conversion at position [[12,936]] 130,474 of ~~SEQ ID NO: 19~~ SEQ ID NO: 18;

(b) an oligonucleotide having a sequence including a genetic polymorphism that is an ~~[[AT]]~~ TA deletion at positions ~~[[15,012-15,013]]~~ 128,398-128,399 of ~~SEQ ID NO: 19~~ SEQ ID NO: 18;

(c) an oligonucleotide having a sequence including a gene polymorphism that is ~~[[A]]~~ T to ~~[[C]]~~ G conversion at position ~~[[16,359]]~~ 127,051 of ~~SEQ ID NO: 19~~ SEQ ID NO: 18;

(d) an oligonucleotide having a sequence including a gene polymorphism that is ~~[[A]]~~ T to ~~[[G]]~~ C conversion at position of ~~[[33,392]]~~ 110,018 of ~~SEQ ID NO: 19~~ SEQ ID NO: 18;

(e) an oligonucleotide having a sequence including a gene polymorphism that is ~~[[A]]~~ T to ~~[[G]]~~ C conversion at position ~~[[47,315]]~~ 96,095 of ~~SEQ ID NO: 19~~ SEQ ID NO: 18;  
and

(f) an oligonucleotide having a sequence including a genetic polymorphism that is ~~[[C]]~~ G deletion ~~[[at]]~~ between positions ~~[[49,053 and 49,054]]~~ 94,356-94,357 of ~~SEQ ID NO: 19~~ SEQ ID NO: 18.

Claim 31 (Cancelled)

Claim 32 (Previously Presented): The method of claim 23, wherein said polymorphism is identified by a method employing a probe or primer selected from the group consisting of:

- (a) an oligonucleotide having the sequence of SEQ ID NO: 3;
- (b) an oligonucleotide having the sequence of SEQ ID NO: 6;
- (c) an oligonucleotide having the sequence of SEQ ID NO: 9;
- (d) an oligonucleotide having the sequence of SEQ ID NO: 12; and
- (f) an oligonucleotide having the sequence of SEQ ID NO: 17.

Claim 33 (Currently Amended): The method of claim 32, which is used to determine the risk of vesnarinone-induced ~~drug-induced~~ granulocytopenia attributed to vesanarinone administration

Claim 34 (Currently Amended): The method of claim 23, wherein said polymorphism is identified by a method employing a probe or primer having a sequence including a gene polymorphism that is  $[[A]] \underline{T}$  to  $[[G]] \underline{C}$  conversion at position  $[[47,315]]$  96,095 of ~~SEQ ID NO: 19~~ SEQ ID NO: 18 and employing the restriction enzyme *Afa* I.

Claim 35 (Currently Amended): The method of claim 34, which is used to determine the risk of vesnarinone-induced ~~drug-induced~~ granulocytopenia attributed to vesanarinone administration

Claim 36 (Currently Amended): A method for examination a subject for the risk of developing vesnarinone-induced ~~drug-induced~~ granulocytopenia comprising the method of claim 32.

Claim 37 (Previously Presented): The method of claim 36, further comprising obtaining a cDNA or genomic DNA sample from said subject.